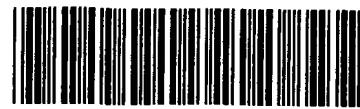# RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/461,537B

Source: 1FW16

Date Processed by STIC: 11/5/04

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17W/6

RAW SEQUENCE LISTING   DATE: 11/05/2004
PATENT APPLICATION: **US/09/461,537B**   TIME: 10:31:39

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Output Set: **N:\CRF4\11052004\I461537B.raw**

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 3 <110> APPLICANT: Novozymes Biotech
 4        Royer, John C
 5        Moyer, Donna L
 6        Yoder, Wendy T
 7        Shuster, Jeffrey R
 9 <120> TITLE OF INVENTION: Non-Toxic, Non-Pathogenic, Non-Pathogenic Fusarium
Expression
10        System
12 <130> FILE REFERENCE: 4216.260-US
14 <140> CURRENT APPLICATION NUMBER: 09/461,537B
15 <141> CURRENT FILING DATE: 1999-12-15
17 <150> PRIOR APPLICATION NUMBER: 08/816,915
18 <151> PRIOR FILING DATE: 1997-03-13
20 <150> PRIOR APPLICATION NUMBER: 08/726,105
21 <151> PRIOR FILING DATE: 1996-10-04
23 <150> PRIOR APPLICATION NUMBER: 08/404,678
24 <151> PRIOR FILING DATE: 1995-03-15
26 <150> PRIOR APPLICATION NUMBER: 08/269,449
27 <151> PRIOR FILING DATE: 1994-06-30
29 <160> NUMBER OF SEQ ID NOS: 16
31 <170> SOFTWARE: PatentIn version 3.2
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 30
35 <212> TYPE: DNA
36 <213> ORGANISM: Fusarium oxysporum
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61 atccccaaca ttgttggtgg cacttctgcc agcgctggcg actttccctt catcgtgagc  180
63 attagccgca acggtggccc ctggtgtgga ggttctctcc tcaacgccaa caccgtcttg  240
65 actgctgccc actgcgtttc cggatacgct cagagcggtt ccagattcg tgctggcagt  300
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87  aagatatgag ttgatttcag ttggatctta gtcctggttg ctcgtaatag agcaatctag   960
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94  <212> TYPE: PRT
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100 <222> LOCATION: (1)..(24)
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104 <222> LOCATION: (25)..(248)
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113             -5              -1  1               5
116 Ala Gly Asp Phe Pro Phe Ile Val Ser Ile Ser Arg Asn Gly Gly Pro
117     10              15              20
120 Trp Cys Gly Gly Ser Leu Leu Asn Ala Asn Thr Val Leu Thr Ala Ala
121 25              30              35                      40
124 His Cys Val Ser Gly Tyr Ala Gln Ser Gly Phe Gln Ile Arg Ala Gly
125             45              50                  55
128 Ser Leu Ser Arg Thr Ser Gly Gly Ile Thr Ser Ser Leu Ser Ser Val
129             60              65                  70
132 Arg Val His Pro Ser Tyr Ser Gly Asn Asn Asn Asp Leu Ala Ile Leu
133         75              80                  85
136 Lys Leu Ser Thr Ser Ile Pro Ser Gly Gly Asn Ile Gly Tyr Ala Arg
137     90              95                  100
140 Leu Ala Ala Ser Gly Ser Asp Pro Val Ala Gly Ser Ser Ala Thr Val
141 105             110             115                     120
144 Ala Gly Trp Gly Ala Thr Ser Glu Gly Gly Ser Ser Thr Pro Val Asn
145             125             130                 135
148 Leu Leu Lys Val Thr Val Pro Ile Val Ser Arg Ala Thr Cys Arg Ala
149             140             145                 150
152 Gln Tyr Gly Thr Ser Ala Ile Thr Asn Gln Met Phe Cys Ala Gly Val
153         155             160                 165
156 Ser Ser Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Ile
157     170             175                 180
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173 <211> LENGTH: 1206
174 <212> TYPE: DNA
175 <213> ORGANISM: Fusarium oxysporum
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182 gcaaagtcct tctagtacct cccaaaactt gatttacgcg ctctccaatc aaaagtacct   180
184 tccaaaagtg atctacctca gctctagatc agggcaccta ttcgcaaaga tctacaagct   240
186 gaactagtaa gcatagcggg agaatatccc acatcattcg agaaggcctt cgtattagac   300
188 ctagtgggat cgacagaaaa gataagacgg agatagatgc tatgtttgga aggtagggga   360
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192 tgacagactg gccacagagg tgtatcctat gcaggtcgat gcgtgcgtta tcgcagggct   480
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198 cagatgcgct ttgatgcttg gcgattcctc gggctaaata actccggttg gtctgtagaa   660
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202 agacacactg tagatcagct cttcgatgac tcttaccagc tttataataa cattcatctt   780
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210 ctagactacg gaacaacgga gcttagtacc agaaaggcag gtacgcctat tcgcaaactc  1020
212 cgaagataca accaagcaag cttatcgcgg gatagtaacc agagaggcag gtaagaagac  1080
214 acaacaacat ccatagctat gtagattctc gaatataaaa ggaccaagat ggactattcg  1140
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231 gcaaagtcct tctagtacct cccaaaactt gatttacgcg ctctccaatc aaaagtacct   180
233 tccaaaagtg atctacctca gctctagatc agggcaccta ttcgcaaaga tctacaagct   240
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237 ctagtgggat cgacagaaaa gataagacgg agatagatgc tatgtttgga aggtagggga   360
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241 tgacagactg gccacagagg tgtatcctat gcaggtcgat gcgtgcgtta tcgcagggct   480
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257 ttatatgccg atcactttca cgggagcatg ataaggttaa tgcttcttct gaatgccgaa    960
259 taaatacctt gttggaagcg tcgagatgtt ccttgaatat tctctagctt gagtcttgga   1020
261 tacgaaacct gtttgagaaa taggtttcaa cgagttaaga agatatgagt tgatttcagt   1080
263 tggatcttag tcctggttgc tcgtaataga gcaatctaga tagcccaaat tgaatatgaa   1140
265 atttgatgga aatattcatt tcgatagaag caacgtgaaa tgtctagcag gacgaaaagt   1200
267 agatcaaggc tgttatgttc cccgaccaac ctaccttgat gtcagtctgc gagtcgtgtg   1260
269 cagtgaccca gaatgatgga ttgacttgga cattttctgt ctatgaagta ttatgaacat   1320
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273 cagtcaagta tctgcgtatg aagggttgtt aagccaggac ggtatcagcg ttgaatattt   1440
275 aaagaatgat atgagataat caacattgac atgataaaag aaaaggggaa acaaattgtg   1500
277 catatagtaa agacttcagg tcgacccctc aatagacata tgcgaaccga aaaccaacag   1560
279 gatacaattt atagataagt ataactacag ttatctgtct gccgaacaaa tactcttttg   1620
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291 tctgctgata gtcctccaac ttctcgaagt cgtaaacgat ggcctatagt atcttattga   1980
293 gaaatatgtc ttctcagaaa attatatctt gtttaccttt cggtccgcca tggctgctaa   2040
295 aactgctggg aaattcaaaa gcgcagcaca agcagcaaga gtgatgggca caacgtgata   2100
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301 <211> LENGTH: 1060
302 <212> TYPE: DNA
303 <213> ORGANISM: Humicola insolens
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308 <222> LOCATION: (10)..(924)
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312 <222> LOCATION: (10)..(72)
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315 <221> NAME/KEY: mat_peptide
316 <222> LOCATION: (73)..(924)
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323 ctg ccg gtg ttg gcc ctt gcc gct gat ggc agg tcc acc cgc tac tgg      99
324 Leu Pro Val Leu Ala Leu Ala Ala Asp Gly Arg Ser Thr Arg Tyr Trp
325           -5                 -1  1                 5
327 gac tgc tgc aag cct tcg tgc ggc tgg gcc aag aag gct ccc gtg aac     147
328 Asp Cys Cys Lys Pro Ser Cys Gly Trp Ala Lys Lys Ala Pro Val Asn
329 10                 15                 20                 25
331 cag cct gtc ttt tcc tgc aac gcc aac ttc cag cgt atc acg gac ttc     195
332 Gln Pro Val Phe Ser Cys Asn Ala Asn Phe Gln Arg Ile Thr Asp Phe
333               30                 35                 40
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335 gac gcc aag tcc ggc tgc gag ccg ggc ggt gtc gcc tac tcg tgc gcc      243
336 Asp Ala Lys Ser Gly Cys Glu Pro Gly Gly Val Ala Tyr Ser Cys Ala
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339 gac cag acc cca tgg gct gtg aac gac gac ttc gcg ctc ggt ttt gct      291
340 Asp Gln Thr Pro Trp Ala Val Asn Asp Asp Phe Ala Leu Gly Phe Ala
341         60              65                  70
343 gcc acc tct att gcc ggc agc aat gag gcg ggc tgg tgc tgc gcc tgc      339
344 Ala Thr Ser Ile Ala Gly Ser Asn Glu Ala Gly Trp Cys Cys Ala Cys
345         75              80                  85
347 tac gag ctc acc ttc aca tcc ggt cct gtt gct ggc aag aag atg gtc      387
348 Tyr Glu Leu Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Val
349 90              95                  100                 105
351 gtc cag tcc acc agc act ggc ggt gat ctt ggc agc aac cac ttc gat      435
352 Val Gln Ser Thr Ser Thr Gly Gly Asp Leu Gly Ser Asn His Phe Asp
353             110                 115                 120
355 ctc aac atc ccc ggc ggc ggc gtc ggc atc ttc gac gga tgc act ccc      483
356 Leu Asn Ile Pro Gly Gly Gly Val Gly Ile Phe Asp Gly Cys Thr Pro
357             125                 130                 135
359 cag ttc ggc ggt ctg ccc ggc cag cgc tac ggc ggc atc tcg tcc cgc      531
360 Gln Phe Gly Gly Leu Pro Gly Gln Arg Tyr Gly Gly Ile Ser Ser Arg
361         140                 145                 150
363 aac gag tgc gat cgg ttc ccc gac gcc ctc aag ccc ggc tgc tac tgg      579
364 Asn Glu Cys Asp Arg Phe Pro Asp Ala Leu Lys Pro Gly Cys Tyr Trp
365         155             160                 165
367 cgc ttc gac tgg ttc aag aac gcc gac aat ccg agc ttc agc ttc cgt      627
368 Arg Phe Asp Trp Phe Lys Asn Ala Asp Asn Pro Ser Phe Ser Phe Arg
369 170             175                 180                 185
371 cag gtc cag tgc cca gcc gag ctc gtc gct cgc acc gga tgc cgc cgc      675
372 Gln Val Gln Cys Pro Ala Glu Leu Val Ala Arg Thr Gly Cys Arg Arg
373             190                 195                 200
375 aac gac gac ggc aac ttc cct gcc gtc cag atc ccc tcc agc agc acc      723
376 Asn Asp Asp Gly Asn Phe Pro Ala Val Gln Ile Pro Ser Ser Ser Thr
377             205                 210                 215
379 agc tct ccg gtc aac cag cct acc agc acc agc acc acg tcc acc tcc      771
380 Ser Ser Pro Val Asn Gln Pro Thr Ser Thr Ser Thr Thr Ser Thr Ser
381         220                 225                 230
383 acc acc tcg agc ccg cca gtc cag cct acg act ccc agc ggc tgc act      819
384 Thr Thr Ser Ser Pro Pro Val Gln Pro Thr Thr Pro Ser Gly Cys Thr
385         235                 240                 245
387 gct gag agg tgg gct cag tgc ggc ggc aat ggc tgg agc ggc tgc acc      867
388 Ala Glu Arg Trp Ala Gln Cys Gly Gly Asn Gly Trp Ser Gly Cys Thr
389 250             255                 260                 265
391 acc tgc gtc gct ggc agc act tgc acg aag att aat gac tgg tac cat      915
392 Thr Cys Val Ala Gly Ser Thr Cys Thr Lys Ile Asn Asp Trp Tyr His
393             270                 275                 280
395 cag tgc ctg tagacgcagg gcagcttgag ggccttactg gtggccgcaa           964
396 Gln Cys Leu
399 cgaaatgaca ctcccaatca ctgtattagt tcttgtacat aatttcgtca tccctccagg  1024
401 gattgtcaca taaatgcaat gaggaacaat gagtac                           1060
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VERIFICATION SUMMARY   DATE: 11/05/2004
PATENT APPLICATION: US/09/461,537B   TIME: 10:31:40

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